

OS79Y4_HUMAN
ID OS79Y4_HUMAN PRELIMINARY; PRT; 317 AA.
AC OS79Y4;
DT 01-FEB-2005 (Tremblrel. 29, Created)
DT 01-FEB-2005 (Tremblrel. 29, Last sequence update)
DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
DE Tumor necrosis factor (ligand) superfamily, member 11 (Fragment).
GN Name=TNFSF11; OSNames=RP11-66N24.2-001;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL139382; CA16926.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
FT NON TER 317
SQ SEQUENCE 317 AA; 35478 MW; 76617646348097P CRC64;
Query Match 100.0%; Score 1685; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 6.5e-136;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRASRDYTKYLRGSEEMGGGAGPHEGFLNAPPPAPHPAPASRSMFALLGLGLGV 60
DB 1 MRASRDYTKYLRGSEEMGGGAGPHEGFLNAPPPAPHPAPASRSMFALLGLGLGV 60
QY 61 VCSVALFFYPRAQMDPNRISDGTCTIRIRIENADPOTTLSSQDTKLIPISSCRIR 120
DB 61 VCSVALFFYPRAQMDPNRISDGTCTIRIRIENADPOTTLSSQDTKLIPISSCRIR 120
QY 121 QAFQAGAVQKELQHTVGSQHTPAEKAMVDGSLDLAKSKLEAPPAHLTTNATDIPSGSH 180
DB 121 QAFQAGAVQKELQHTVGSQHTPAEKAMVDGSLDLAKSKLEAPPAHLTTNATDIPSGSH 180
QY 181 KVLSSWYHNRGNAKTSNMTFSPNGKLIIVNDGFFYLYANICFRHETSGDLATEYLQLMV 240
DB 181 KVLSSWYHNRGNAKTSNMTFSPNGKLIIVNDGFFYLYANICFRHETSGDLATEYLQLMV 240
QY 241 YVTKTSIKIPSSHTLKKSGSTKXSGSEFHFPIYINVGFFPKLRSGEISIEVSNPSILD 300
DB 241 YVTKTSIKIPSSHTLKKSGSTKXSGSEFHFPIYINVGFFPKLRSGEISIEVSNPSILD 300
QY 301 PQDQATYFGAFKVRDID 317
DB 301 PQDQATYFGAFKVRDID 317

RESULT 3

TNFI_MOUSE
ID TNFI_MOUSE STANDARD; PRT; 316 AA.
AC OS3235; OS35306; OSJUK8; OSJUK9; OSR110;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-inducing cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF) (Contains: Tumor necrosis factor ligand superfamily member 11, soluble form); Tumor necrosis factor ligand superfamily member 11, soluble form.
GN Name=TNF11; Synonyms=Opgl, Rankl, Trance;
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]

RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC TISSUE=Hybridoma;
RX MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
RA Wong B.R., Rno J., Arion J., Robinson E., Orlicki J., Chao M.,
RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA Choi Y.;
RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates C-Jun N-terminal kinase in T cells.";
RL J. Biol. Chem. 272:25190-25194(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC TISSUE=Thymic Lymphoma;
RX MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougan W.C.,
RA Tomersko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
RL Nature 390:175-179(1997).
RN [3]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC TISSUE=Bone marrow;
RX MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
RA Lacey D.L., Timme E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA Sullivan J., Hawkins N., Davy E., Capparelli C., Ri A., Qian Y.-X.,
RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA Boyle W.J.;
RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation.";
RL Cell 93:165-176(1998).
RN [4]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC TISSUE=Bone marrow stroma;
RX MEDLINE=98188248; PubMed=9520411; DOI=10.1073/pnas.95.7.3597;
RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,
RA Mochizuki S.-I., Tomiyasu A., Yano K., Goto M., Murakami A., Tada E.,
RA Motomura T., Higashio K., Udagawa N., Takahashi N., Suda T.;
RT "Osteoclast differentiation factor is a ligand for osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical to TRANCE/RANKL.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
RN [5]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC STRAIN=129;
RX MEDLINE=99214075; PubMed=10196481; DOI=10.1016/S0378-1119(99)00025-6;
RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
RA Ueda M., Higashio K.;
RT "Cloning and characterization of the gene encoding mouse osteoclast differentiation factor.";
RL Gene 230:121-127(1999).
RN [6]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1, 2 AND 3).
RX MEDLINE=21150053; PubMed=11250921; DOI=10.1210/en.142.4.1419;
RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
RT "Determination of three isoforms of the receptor activator of nuclear factor-kappaB ligand and their differential expression in bone and thymus.";
RL Endocrinology 142:1419-1426(2001).
RN [7]
RP PROTEIN SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.
RX MEDLINE=99240759; PubMed=10224132; DOI=10.1074/jbc.274.19.13613;
RA Lum L., Wong B.R., Josien R., Becherer J.D., Edjument-Bromage H.,
RA Schloendorff J., Tempst P., Choi Y., Blobel C.P.;
RT "Evidence for a role of a tumor necrosis factor- α 1pha (TNF- α 1pha) -member involved in osteoclastogenesis and dendritic cell survival.";
RL J. Biol. Chem. 274:13613-13618(1999).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.
RX MEDLINE=21464816; PubMed=11581298;
RA Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;
RT "Crystal structure of the TRANCE/RANKL cytokine reveals determinants

DR	InterPro; IPRO03636; TNF_subf.
DR	Pfam; PF00229; TNF; 1.
DR	ProDom; PD002012; TNF_subf; 1.
DR	SMART; SMO0207; TNF; 1.
DR	PROSITE; PS00251; TNF_1; FALSE_NEG.
DR	PROSITE; PS00049; TNF_2; 1.
KM	3d-structure; Alternative splicing; Cytokine; Developmental protein;
KW	Differentiation; Direct protein sequencing; Glycoprotein; Receptor;
KW	Signal-anchor; Transmembrane.
FT	CHAIN 1 316
FT	Tumor necrosis factor ligand superfamily member 11, membrane form.
FT	member 11, soluble form.
FT	Cytoplasmic (Potential).
FT	Signal-anchor for type II membrane protein (Potential).
FT	Extracellular (Potential).
FT	Cleavage.
FT	N-linked (GlcNAc..) (Potential).
FT	N-linked (GlcNAc..) (Potential).
FT	Missing (in isoform 3).
FT	/PrideVSP_006448.
FT	SSEMSGGGVPEHGPALPAPSAAPPAPPA -> TP (in isoform 2).
FT	/PrideVSP_006449.
FT	G -> D (in Ref. 2).
FT	Missing (in Ref. 5).
FT	VARSPIC 14 44
FT	CONFLICT 99 99
FT	CONFLICT 141 143
FT	STRAND 164 169
FT	TURN 171 172
FT	STRAND 181 182
FT	STRAND 186 187
FT	TURN 191 192
FT	STRAND 194 196
FT	STRAND 198 201
FT	TURN 202 203
FT	STRAND 204 207
Query Match	84.1%; Score 1417.5; DB 1; Length 316;
Best Local Similarity	84.3%; Pred No. 5.7e-113;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2	
QY	1 MRASRDYTKYLRSSENGGGPGAPHEGPLH-APPAPPHOPAPASRSMFYALGLIGQ 59
DB	1 MRASRDYGKYLRSSENGSGGVHBEPLPAPSAPAPAPASRSMFLALGLIGQ 60
QY	60 VVCSTALFFYRAQMDPNRISEDGTHCIYRLRLHENADFDOTLTESODTSLIPDSCHRI 119
DB	61 VVCSTALFLYRAQMDPNRISESDSTHCYFIRLRHENAGLDSTLESBDT--LDSCRM 118
QY	120 KOAFQGAQOKELOHVVSQHTRAEKANWDGSWLMLAKSKLEAOPFAHLTNATDIPSGS 179
DB	119 KOAFQGAQOKLOHIHVGFORPSGAPAMMEGSSWLDVAORGREAOFPALHTINNASIPSGS 178
QY	180 HKVLSSWYHDGRGNAKISNMTFSNGKLIVNODGYFYLYANICPRHHETSGDLATERYQLM 239
DB	179 HKVTLSWYHDGRGNAKISNMTLSNGKLAVNODGYFYLYANICRRHETSQSVPTDYQLM 238
QY	240 VYVTKTSIKLPSSHTLMKGSGSTKYWSNFHFYSINVGGFFPKLRSGEISIEVSNPSLL 299
DB	239 VYVVKTSIKLPPSSHNLKKGSTKYWSNSFHFIYSINVGGFFPLRAGEISIQVSNPSLL 298
QY	300 DPDDATYPGAPKVRDID 317
DB	299 DPDDATYPGAPKVRDID 316
RESULT 4	
ID	TNFI RAT STANDARD; PRT; 318 AA.
AC	QPSSEZ; Q91Z19;
DT	28-FEB-2003 (Rel. 41, Created)
DT	28-FEB-2003 (Rel. 41, Last sequence update)
DT	13-SEP-2005 (Rel. 48, Last annotation update)

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FT      TURN      202      203
FT      STRAND      204      207

Query Match      100.0%; Score 148; DB 1; Length 316;
Best Local Similarity 100.0%; Pred. No. 2.1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NAASIPSGSHKVTLSWYHGRGMAKIS 27
DB      170 NAASIPSGSHKVTLSWYHGRGMAKIS 196

RESULT 2
TNF1L_RAT
ID      TNF1L_RAT      STANDARD;      PRT;      318 AA.
AC      Q9SESE2; Q91219;
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      13-SEP-2005 (Rel. 48, Last annotation update)
DE      Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE      of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE      induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE      differentiation factor) (ODF) [contains: Tumor necrosis factor ligand
DE      superfamily member 11, membrane form; Tumor necrosis factor ligand
DE      superfamily member 11, soluble form].
GN      Name=Tnf1l; Synonyms=Oppl, Rankl, Trance;
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
[1]
RN      NUCLEOTIDE SEQUENCE.
RP      TISSUE=Tibial bone;
RX      MEDLINE=20540945; PubMed=11092398;
RA      Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,
RA      Zheng M.H.;
RT      "Cloning, sequence and functional characterization of the rat
RT      homologue of receptor activator of NF-kB ligand.";
RL      J. Bone Miner. Res. 15:2178-2186(2000).
RN      [2]
RP      NUCLEOTIDE SEQUENCE OF 266-318.
RC      STRAIN=Fischer 344;
RX      MEDLINE=21662371; PubMed=11804028;
RA      Odgren P.R., Kim N., van Wesenbeeck L., Mackay C., Mason-Savay A.,
RA      Safadi F.F., Popoff S.N., Lengner C., van-Hul W., Choi Y.,
RA      Marks S.C. Jr.;
RT      "Evidence that the rat osteopetrotic mutation toothless (tl) is not in
RT      the TNFRSF11 (TRANCE, RANKL, ODF, OPGL) gene.";
RL      Int. J. Dev. Biol. 45:853-859(2001).
CC      -1- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
CC      TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC      Augments the ability of dendritic cells to stimulate naive T-cell
CC      proliferation. May be an important regulator of interactions
CC      between T cells and dendritic cells and may play a role in the
CC      regulation of the T cell-dependent immune response. May also play
CC      an important role in enhanced bone resorption in humoral
CC      hypercalcemia of malignancy.
CC      -1- SUBUNIT: Homodimer (By similarity).
CC      -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC      similarity).
CC      -1- TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.
CC      -1- PTM: The soluble form derives from the membrane form by
CC      proteolytic processing (By similarity).
CC      -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC
CC      EMBL, AF187319; AAC17031.1; -, mRNA.

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DR      EMBL; AF425669; AAL23963.1; -, mRNA.
DR      HSSP; O35235; 1J7Z.
DR      SMR; Q9SESE2; 163-318.
DR      Ensembl; ENSRNOG0000009559; Rattus norvegicus.
DR      RGD; 620784; Tnf1l.
DR      GO; GO:0045780; P:positive regulation of bone resorption; IMP.
DR      GO; GO:0045672; P:positive regulation of osteoclast different. . .; IMP.
DR      InterPro; IPR006052; TNF_family.
DR      InterPro; IPR003636; TNF_subf.
DR      Pfam; PF00229; TNF; 1.
DR      ProDom; PD002012; TNF_subf; 1.
DR      SMART; SM00207; TNF; 1.
DR      PROSITE; PS00251; TNF_1; FALSE_NEG.
DR      CYTOKINE; Developmental protein; Differentiation; Glycoprotein;
DR      Receptor; Signal-anchor; Transmembrane.
FT      CHAIN      1      318
FT
FT      CHAIN      141      318
FT
FT      TOPO_DOM      1      47
FT      TRANSMEM      48      68
FT
FT      TOPO_DOM      69      318
FT      SITE      140      141
FT      CARBOHYD      199      199
FT      CARBOHYD      264      264
FT      CONFLICT      317      317
FT      SEQUENCE      318 AA; 35370 MW; 4B87A4D706AD098F CRC64;
QY      1 NAASIPSGSHKVTLSWYHGRGMAKIS 27
DB      172 NAADIPSGSHKVTLSWYHGRGMAKIS 198

Query Match      94.6%; Score 140; DB 1; Length 318;
Best Local Similarity 92.6%; Pred. No. 2.8e-11;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 NAASIPSGSHKVTLSWYHGRGMAKIS 27
DB      172 NAADIPSGSHKVTLSWYHGRGMAKIS 198

RESULT 3
Q54A98 HUMAN
ID      Q54A98 HUMAN PRELIMINARY;      PRT;      244 AA.
AC      O54A98;
DT      13-SEP-2005 (TrEMBLrel. 31, Created)
DT      13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT      13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE      Receptor activator of nuclear factor kappa B ligand 3.
GN      Name=hRANKL 3;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC      Homo.
OX      NCBI_TaxID=9606;
[1]
RN      NUCLEOTIDE SEQUENCE.
RP      PubMed=14751235; DOI=10.1016/j.birc.2003.12.191;
RA      Suzuki J., Ikeda T., Kuroyama H., Seki S., Kasai M., Utsuyama M.,
RA      Tatsumi M., Dematsu H., Hirokawa K.;
RT      "Regulation of osteoclastogenesis by three human RANKL isoforms
RT      expressed in NIH3T3 cells.";
RL      Biochem. Biophys. Res. Commun. 314:1021-1027(2004).
DR      EMBL; AB064268; BAB79693.1; -, mRNA.
KW      Receptor.
SQ      SEQUENCE      244 AA; 27690 MW; C827590684B8B3C CRC64;
QY      1 NAASIPSGSHKVTLSWYHGRGMAKIS 27
DB      98 NAADIPSGSHKVTLSWYHGRGMAKIS 124

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FT TURM 202 203
FT STRAND 204 207

Query Match 100.0%; Score 84; DB 1; Length 316;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VVVVTSIKIPSSHML 17
DB 239 VVVVTSIKIPSSHML 255

RESULT 2
ID TNF11 RAT STANDARD; PRT; 318 AA.

AC Q9SEB2; Q91Z19; (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 11 (receptor activator
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE differentiation factor) (ODF) [Contains: Tumor necrosis factor ligand
DE superfamily member 11, membrane form; Tumor necrosis factor ligand
DE superfamily member 11, soluble form].
GN Name=TNF11; Synonyms=Oppl, Rankl, Trance;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 11
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Tibial bone;
RX MEDLINE=20540945; PubMed=11092398;
RA Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,
RA Zheng M.H.;
RT "Cloning, sequence and functional characterization of the rat
RT homologue of receptor activator of NF-kB ligand.";
RL J. Bone Miner. Res. 15:2178-2186(2000).
[2]
RN NUCLEOTIDE SEQUENCE OF 266-318.
RP STRAIN=Flischer 344;
RX MEDLINE=21662371; PubMed=11804028;
RA Osdoren P.R., Kim N., van Wesenbeeck L., Mackay C., Mason-Savvas A.,
RA Safadi F.P., Popoff S.N., Lengner C., van-Hul W., Choi Y.,
RA Marks S.C. Jr.;
RT "Evidence that the rat osteopetrotic mutation toothless (tl) is not in
RT the TNFSF11 (TRANCE, RANKL, ODF, OPGL) gene.";
RL Int. J. Dev. Biol. 45:853-859(2001).
CC -1- FUNCTION: Cytokine that binds to TNFSF11B/OPG and to
CC TNFSF11A/RANK. Osteoclast differentiation and activation factor.
CC Augments the ability of dendritic cells to stimulate naive T-cell
CC proliferation. May be an important regulator of interactions
CC between T cells and dendritic cells and may play a role in the
CC regulation of the T cell-dependent immune response. May also play
CC an important role in enhanced bone-resorption in humoral
CC hypercalcaemia of malignancy.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC similarity).
CC -1- TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL, AF187319; AAG17031.1; -, mRNA.

DR EMBL; AF425669; AAL23963.1; -, mRNA.
DR HSSP; O35235; 1J72.
DR SMR; Q9SEB2; 163-318.
DR Ensembl; ENSRNOG0000009559; Rattus norvegicus.
DR RGD; 620784; Tnf11.
DR GO; GO:0045780; P:positive regulation of bone resorption; IMP.
DR GO; GO:0045672; P:positive regulation of osteoclast different. . .; IMP.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; FALSE_NEG.
DR PROSITE; PS00409; TNF_2; 1.
KW Cytokine; Developmental protein; Differentiation; Glycoprotein;
KW Receptor; Signal-anchor; Transmembrane.
FT CHAIN 1 318
FT CHAIN 141 318
FT TOPO_DOM 1 47
FT TRANSMEM 48 68
FT FT
FT TOPO_DOM 69 318
FT SITE 140 141
FT CARBOHYD 199 199
FT CARBOHYD 264 264
FT CONFLICT 317 317
SQ SEQUENCE 318 AA; 35370 MW; 4B87AD706AD098F CRC64;

Query Match 100.0%; Score 84; DB 1; Length 318;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VVVVTSIKIPSSHML 17
DB 241 VVVVTSIKIPSSHML 257

RESULT 3
ID 054A98 HUMAN PRELIMINARY; PRT; 244 AA.
AC 054A98;
DT 13-SEP-2005 (TRENBLREL. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLREL. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLREL. 31, Last annotation update)
DE Receptor activator of nuclear factor kappa B ligand 3.
GN Name=hRANKL 3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN 11
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14751235; DOI=10.1016/j.birc.2003.12.191;
RA Suzuki J., Ikeda T., Kuroyama H., Seki S., Kasai M., Utsuyama M.,
RA Tatematsu M., Uematsu H., Hirokawa K.;
RT "Regulation of osteoclastogenesis by three human RANKL isoforms
RT expressed in NIH3T3 cells.";
RL Biochem. Biophys. Res. Commun. 314:1021-1027(2004).
DR EMBL; AB064266; BAB79693.1; -, mRNA.
KW Receptor.
SQ SEQUENCE 244 AA; 27690 MW; C827590684B6B83C CRC64;

Query Match 88.1%; Score 74; DB 2; Length 244;
Best Local Similarity 88.2%; Pred. No. 0.00015;
Matches 15, Conservative 0, Mismatches 2, Indels 0, Gaps 0;

QY 1 VVVVTSIKIPSSHML 17
DB 167 VVVVTSIKIPSSHML 183